



#11

## SEQUENCE LISTING

&lt;110&gt; Barber, Elizabeth K

&lt;120&gt; Gene Expression Control Element DNA

&lt;130&gt; 896034605001

&lt;140&gt; US/09/966,264C

&lt;141&gt; 2001-09-28

&lt;150&gt; US/60/237,079

&lt;151&gt; 2000-09-30

&lt;160&gt; 61

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 137

&lt;212&gt; DNA

&lt;213&gt; human

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Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu  
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tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95  
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys  
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taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
      Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
              20              25              30

atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
              35              40              45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192
Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala      His
              50              55              60

ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
Phe Ser Met      Thr Pro Val Ala      Ser Asn Ile Lys Leu Ile Leu
              65              70              75

aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
Thr Asn Asn Val      Trp Leu His      Gly Phe Ala Ser Ser Trp
              80              85

aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
          90              95              100

ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
105              110              115              120

gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
Glu Thr Glu      Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
              125              130              135

ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
              140              145              150

gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
              155              160              165
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gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576  
 Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His  
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ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624  
 Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe  
 185 190 195

aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672  
 Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys  
 200 205 210

aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720  
 Arg Phe Gln Phe Leu Ser Leu Leu Leu Phe Cys Gln Trp Gln  
 215 220 225

gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768  
 Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr  
 230 235 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816  
 Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr  
 245 250 255

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 His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr  
 260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912  
 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr  
 275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960  
 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg  
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          20           25           30
Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys
          35           40           45
Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln
          50           55           60
Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe
65           70           75           80
Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg
          85           90           95
Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser
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Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile
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Gly	Asn	Leu	Asn	Val	Ala	Arg	His	Phe	Ser	Met	Lys	Thr	Pro	Val	Ala
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Arg	Ser	Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His
65					70				75					80	

Lys	Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu
				85				90						95	

Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu	Met
			100					105					110		

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser  
 115 120 125  
 Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His  
 130 135 140  
 Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met  
 145 150 155 160  
 Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met  
 165 170 175  
 Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr  
 180 185 190  
 Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu  
 195 200 205  
 Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu  
 210 215 220  
 Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val  
 225 230 235 240  
 Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys  
 245 250 255  
 Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu  
 260 265 270  
 Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn  
 275 280 285  
 Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn  
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 Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser  
 20 25 30  
 acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144  
 Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys  
 35 40 45  
 aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192  
 Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly  
 50 55 60  
 tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 234  
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Gly Arg Asn Ser Met Arg Ser Arg Val  
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Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr  
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Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala  
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Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu Leu  
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Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu  
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35 40 45

Glu Glu Gly Ala Glu  
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ttt att att att att ttc aac cca agt aaa agc aga gag aaa ata gcc 93  
 Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala  
 -60 -55 -50

acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg 141  
 Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu  
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 Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr  
 -30 -25 -20

gat ggt tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 237  
 Trp Val Leu Val Met Val Val Val Val Lys Val Val Met Asp Gly  
 -15 -10 -5

gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 285  
 Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu  
 1 5 10 15

taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 333  
 Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro  
 20 25 30

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 Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly

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			50					55					60							
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				65					70						75					
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Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp					
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Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu					
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105					110					115					120					
gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt	669				
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ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg	717				
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gca	gat	gat	ttg	ggc	aga	gcg	atg	gag	tcc	tta	gta	tca	gtc	atg	aca	765				
Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr					
			155					160					165							
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			170					175						180						
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aga	ttt	cag	tag	ttt	cta	agt	ctg	tta	ttg	ttt	tgt	taa	caa	tgg	cag	957				
Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln					
				215					220						225					
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Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr					
				230					235					240						
tgt	aaa	atc	ttg	ata	gct	aaa	taa	ctt	gcc	att	tct	tta	tat	gga	acg	1053				
Cys	Lys	Ile	Leu	Ile	Ala	Lys		Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr					
			245						250					255						

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 His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr  
 260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 1149  
 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr  
 275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 1197  
 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg  
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 <213> human

<400> 52

Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe  
 1 5 10 15

Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala  
 20 25 30

Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala  
 35 40 45

Leu Lys

<210> 53  
 <211> 32  
 <212> PRT  
 <213> human

<400> 53

Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp  
 1 5 10 15

Gly Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met  
 20 25 30

Val Val

<210> 54  
 <211> 1044

<212> DNA

<213> mouse

<400> 54

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ccaacaaagt gtgaaagggtg tgtgccatta cacatctttc tcggtgataa 200
gagccttgct tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250
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tactaacacc atgcaatgct tcattaacaa ggatttgctt cttgctagaa 350
atgggtaaaa acggactgtg gtctgtatac cttcaatgca gcttatgtgt 400
tgtcttttcc tgaaatggta atgactccca atagtggcaa ccaggggtac 450
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tatggaacgc attttgggtt gtttaaaaat ttataacagt tataaagaaa 900
gattgtaaac taaagtgtgc ttataaaaaa aagttgttta taaaaacccc 950
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<210> 55

<211> 1234

<212> DNA

<213> human

<400> 55

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agttgggtgtg gcggtgatgg tggcagtgat aatgggtgacc gatgggtggg 200
tgctgggtgat ggtagtggta gttgtgaagg tgggtgatggt ggtttgattg 250
atagtaaaaa aaatgttcgt taatacaagt agagagtaag taatcaatca 300
atcactcata gccagggtgg aaaagatgta tcccatcatg gaatattcct 350
gttctgatag aaatcttctg cttatctatg gaattctttt gatatatatt 400
tacattggga acctgaatgt agcttgacat ttttccatgt aaacaccagt 450
agcctgatcc aacattaagc tgatactaac aaacaacgtg taatggcttc 500
attaataagg ctttgccttc tcttggaac tggtgaaaaa tcaaaccctg 550
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gaatgatttc ccaaaggca aagaaacaga gtgatgctat ctatctgcac 650
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<210> 56

<211> 303

<212> PRT

<213> human

<400> 56

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				20					25					30
Asn	Val	Ala	Arg	His	Phe	Ser	Met	Lys	Thr	Pro	Val	Ala	Arg	Ser
				35					40					45
Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His	Lys
				50					55					60
Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu
				65					70					75
Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu
				80					85					90
Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr
				95					100					105
Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	Leu	Ser	Leu	Cys	Phe
				110					115					120
Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu
				125					130					135
Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu
				140					145					150
Gly	Ala	Glu	Lys	Met	Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe
				155					160					165
Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr
				170					175					180
Arg	Asn	Lys	Ser	Ile	Phe	Leu	Arg	Arg	Val	Val	Val	Leu	Tyr	Cys
				185					190					195
Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys	Lys	Gln	Trp
				200					205					210
Gln	Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys
				215					220					225
Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	Leu	Ala	Ile	Ser	Leu
				230					235					240
Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	Lys	Gln	Leu	Lys
				245					250					255
Arg	Lys	Asn	Tyr	Lys	Gly	Lys	Arg	Lys	Lys	Arg	Asn	Gly	Gln	Val
				260					265					270

Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro  
275 280 285

Lys Pro Lys Arg Gly arg Asn Ser Met Arg Ser Arg Val Arg Cys  
290 295 300

Lys Leu Ile

<210> 57

<211>

111

<212> DNA

<213> human

<400> 57

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<210> 58

<211> 260

<212> DNA

<213> human

<400> 58

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AACATCAAAC ACGGCTTCTC ATGCTATTTT TACCTCACTT TGGTTTTGGG 100  
GTGTTCCCTGA TAATTGTGCA CACCTGAGTT CACAGCTTCA CCACTTGTCC 150  
ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTTT CCTTCATAAT 200  
TAACAGTTAT AAAGAAAGAA TTATAAAGGA AAAAGAAAAT AACGCAATGG 250  
ACAAGTGGTG 260

<210> 59

<211> 17

<212> DNA

<213> human



<400> 59

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17

<210> 60

<211> 17

<212> DNA

<213> human

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gcggtgatgg tggcagt

17

<210> 61

<211> 107

<212> PRT

<213> human

<400> 61

Met	Tyr	Pro	Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val
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Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25				30	

Asn	Met	Lys	Lys	Glu	Gln	Asn	Lys	Cys	Phe	Thr	Thr	Pro	Asp	Ser
				35					40				45	

Arg	Met	Val	Phe	Ile	Ile	Phe	Ile	Gln	Gln	Arg	Gly	Leu	Asp	Ser
				50					55				60	

Lys	Ser	Leu	Gln	Glu	Ile	Asn	Leu	Tyr	Phe	Cys	Glu	Gly	Phe	Tyr
				65					70				75	

Thr	Ser	Met	Gln	Leu	Tyr	Lys	Lys	Val	Ile	Arg	Lys	Leu	His	Lys
				80					85				90	

Ile	Thr	Gln	Trp	Thr	Arg	Thr	Pro	Gln	Asn	Gln	Ser	Glu	Val	Glu
				95					100				105	

Ile Ala